

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 10, 2006, 18:27:29 ; Search time 401 Seconds  
(without alignments)  
571.787 Million cell updates/sec

Title: US-10-729-571B-2  
Perfect score: 1315  
Sequence: 1 MKIGVFD SGVGGFSVLKSL.....FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10729571/runat\_09022006\_102157\_17424/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss05p  
-USER=US10729571\_@CGN\_1\_1\_335\_@runat\_09022006\_102157\_17424 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq1:\*  
8: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq3:\*  
11: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq4:\*

12: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		Query		DB		ID	Description
No.	Score	Match	Length				
c 1	1207	91.8	5925	7	US-10-615-668-4		Sequence 4, Appli
2	357	27.1	861	11	US-11-098-686-9767		Sequence 9767, Ap
c 3	357	27.1	1457619	11	US-11-098-686-8739		Sequence 8739, Ap
4	338	25.7	978	7	US-10-467-657-7223		Sequence 7223, Ap
5	201.5	15.3	2887	11	US-11-194-246-237		Sequence 237, App
c 6	136	10.3	200	11	US-11-098-686-6831		Sequence 6831, Ap
c 7	126.5	9.6	200	11	US-11-098-686-6830		Sequence 6830, Ap
c 8	106	8.1	200	11	US-11-098-686-6829		Sequence 6829, Ap
c 9	97	7.4	1802	11	US-11-133-690A-2		Sequence 2, Appli
10	92	7.0	3003	7	US-10-793-626-4040		Sequence 4040, Ap
c 11	92	7.0	3835	7	US-10-793-626-3433		Sequence 3433, Ap
c 12	89.5	6.8	684	7	US-10-750-185-61821		Sequence 61821, A
c 13	89.5	6.8	684	7	US-10-750-623-61821		Sequence 61821, A
14	89	6.8	756	7	US-10-793-626-297		Sequence 297, App
15	89	6.8	756	7	US-10-793-626-721		Sequence 721, App
16	85.5	6.5	600	7	US-10-750-185-3489		Sequence 3489, Ap
17	85.5	6.5	600	7	US-10-750-623-3489		Sequence 3489, Ap
18	85	6.5	2592	7	US-10-793-626-2009		Sequence 2009, Ap
c 19	85	6.5	3242	7	US-10-793-626-4267		Sequence 4267, Ap
20	85	6.5	4103	7	US-10-793-626-3532		Sequence 3532, Ap
21	83.5	6.3	2067	11	US-11-098-686-9498		Sequence 9498, Ap
22	83	6.3	1521	7	US-10-957-569-34		Sequence 34, Appl
23	83	6.3	1521	11	US-11-097-589-32		Sequence 32, Appl
c 24	81.5	6.2	1524	7	US-10-467-657-3485		Sequence 3485, Ap
25	81.5	6.2	1524	7	US-10-467-657-6927		Sequence 6927, Ap
26	81.5	6.2	2058	11	US-11-136-527-758		Sequence 758, App
27	81	6.2	6934	11	US-11-091-883-191		Sequence 191, App
c 28	80	6.1	1272	11	US-11-098-686-9719		Sequence 9719, Ap
c 29	80	6.1	2993	7	US-10-793-626-3821		Sequence 3821, Ap
c 30	80	6.1	31320	7	US-10-995-561-13309		Sequence 13309, A
31	79.5	6.0	1275	7	US-10-793-626-2295		Sequence 2295, Ap
c 32	79.5	6.0	3227	7	US-10-793-626-4111		Sequence 4111, Ap
33	78.5	6.0	3842	7	US-10-793-626-3715		Sequence 3715, Ap
c 34	78.5	6.0	6126	7	US-10-775-169-286		Sequence 286, App
35	78	5.9	2110	7	US-10-510-386-189		Sequence 189, App
36	78	5.9	3053	7	US-10-793-626-3389		Sequence 3389, Ap
c 37	78	5.9	5918	11	US-11-136-527-2279		Sequence 2279, Ap
38	77.5	5.9	12797	7	US-10-995-561-13435		Sequence 13435, A
39	77.5	5.9	14113	7	US-10-995-561-13405		Sequence 13405, A
40	77.5	5.9	98560	7	US-10-995-561-13323		Sequence 13323, A
41	77	5.9	1606	7	US-10-750-185-61279		Sequence 61279, A
42	77	5.9	1606	7	US-10-750-623-61279		Sequence 61279, A
c 43	77	5.9	2935	7	US-10-750-185-49494		Sequence 49494, A
c 44	77	5.9	2935	7	US-10-750-623-49494		Sequence 49494, A
45	76.5	5.8	2449	11	US-11-136-527-2124		Sequence 2124, Ap

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 10, 2006, 18:11:39 ; Search time 201 Seconds  
(without alignments)  
2255.116 Million cell updates/sec

Title: US-10-729-571B-2  
Perfect score: 1315  
Sequence: 1 MKIGVFD SGVGGF SVLKSL.....FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10729571/runat\_09022006\_102153\_17326/app\_query.fasta\_1  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss03h -USER=US10729571@CGN\_1\_1\_193 @runat\_09022006\_102153\_17326  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

		%					
Result		Score	Query Match	Length	DB	ID	Description
No.							
	1	1210	92.0	10299	2	US-08-477-451-5	Sequence 5, Appli
c	2	1207	91.8	5925	3	US-08-470-260-4	Sequence 4, Appli
c	3	1207	91.8	5925	3	US-08-471-491-4	Sequence 4, Appli
c	4	1207	91.8	5925	3	US-08-466-662-4	Sequence 4, Appli
c	5	1207	91.8	10299	2	US-08-477-451-1	Sequence 1, Appli
c	6	1207	91.8	19932	2	US-08-477-451-25	Sequence 25, Appl
	7	360	27.4	810	3	US-09-134-001C-1016	Sequence 1016, Ap
	8	325	24.7	816	3	US-09-902-540-2612	Sequence 2612, Ap
	9	325	24.7	15338	3	US-09-902-540-1121	Sequence 1121, Ap
	10	312	23.7	678	3	US-09-107-433-1466	Sequence 1466, Ap
	11	312	23.7	792	2	US-08-759-907-1	Sequence 1, Appli
	12	312	23.7	792	2	US-08-759-907-3	Sequence 3, Appli
	13	312	23.7	792	3	US-09-303-272-1	Sequence 1, Appli
	14	312	23.7	792	3	US-09-303-272-3	Sequence 3, Appli
	15	312	23.7	9707	3	US-08-961-527-164	Sequence 164, App
	16	309	23.5	795	3	US-09-583-110-301	Sequence 301, App
c	17	298.5	22.7	36470	3	US-08-311-731A-123	Sequence 123, App
	18	288.5	21.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	19	288.5	21.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	20	261	19.8	894	3	US-09-328-352-3915	Sequence 3915, Ap
	21	249	18.9	66986	3	US-09-596-002-29	Sequence 29, Appl
c	22	248.5	18.9	2704	3	US-09-221-017B-94	Sequence 94, Appl
	23	234	17.8	640681	3	US-09-790-988-1	Sequence 1, Appli
	24	233	17.7	972	3	US-09-252-991A-13994	Sequence 13994, A
	25	222.5	16.9	900	3	US-09-543-681A-4127	Sequence 4127, Ap
	26	222	16.9	381	3	US-09-107-532A-1539	Sequence 1539, Ap
	27	217	16.5	885	3	US-09-489-039A-4986	Sequence 4986, Ap
	28	205.5	15.6	1365	3	US-08-956-171E-395	Sequence 395, App
	29	205.5	15.6	1365	3	US-08-781-986A-395	Sequence 395, App
c	30	191.5	14.6	1830121	3	US-09-557-884-1	Sequence 1, Appli
c	31	191.5	14.6	1830121	3	US-09-643-990A-1	Sequence 1, Appli
c	32	191.5	14.6	1830121	3	US-10-158-865-1	Sequence 1, Appli
	33	186	14.1	273	3	US-09-134-000C-2672	Sequence 2672, Ap
	34	171	13.0	786	3	US-09-830-230A-399	Sequence 399, App
	35	151	11.5	573	3	US-09-134-000C-2670	Sequence 2670, Ap
c	36	140	10.6	372	3	US-09-252-991A-14231	Sequence 14231, A
	37	134	10.2	708	3	US-09-830-230A-400	Sequence 400, App
	38	128.5	9.8	636	3	US-09-328-352-869	Sequence 869, App
	39	126	9.6	654	3	US-09-252-991A-14079	Sequence 14079, A
c	40	125	9.5	270	3	US-09-107-532A-2606	Sequence 2606, Ap
c	41	121	9.2	222	3	US-09-134-000C-2671	Sequence 2671, Ap
	42	118.5	9.0	735	3	US-09-107-532A-1648	Sequence 1648, Ap
	43	101.5	7.7	2247	3	US-09-543-681A-2504	Sequence 2504, Ap
	44	100.5	7.6	1400	2	US-08-305-764C-57	Sequence 57, Appl
	45	100.5	7.6	1400	2	US-08-305-764C-59	Sequence 59, Appl

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 10, 2006, 17:54:20 ; Search time 3842 Seconds  
(without alignments)  
3772.795 Million cell updates/sec

Title: US-10-729-571B-2  
Perfect score: 1315  
Sequence: 1 MKIGVFD SGVGGF SVLKSL ..... FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10729571/runat\_09022006\_102149\_17235/app\_query.fasta\_1  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p  
-USER=US10729571\_@CGN\_1\_1\_7415\_@runat\_09022006\_102149\_17235 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*

13: gb\_vi:\*  
 14: gb\_htg:\*  
 15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	1315	100.0	768	6	CQ846366	CQ846366 Sequence
c	2	1315	100.0	10781	1	AE001483	AE001483 Helicobac
	3	1257	95.6	768	6	CQ846368	CQ846368 Sequence
c	4	1249	95.0	26276	1	AY330643S2	AY330644 Helicobac
	5	1248	94.9	765	6	CQ846398	CQ846398 Sequence
	6	1248	94.9	768	6	CQ846384	CQ846384 Sequence
c	7	1248	94.9	11141	1	AE000569	AE000569 Helicobac
	8	1246	94.8	768	6	CQ846386	CQ846386 Sequence
c	9	1245	94.7	26663	1	AY330638S2	AY330639 Helicobac
	10	1240	94.3	768	6	CQ846392	CQ846392 Sequence
c	11	1238	94.1	26771	1	AY330636S2	AY330637 Helicobac
	12	1237	94.1	768	6	CQ846370	CQ846370 Sequence
	13	1237	94.1	768	6	CQ846388	CQ846388 Sequence
c	14	1237	94.1	20229	1	AF282853	AF282853 Helicobac
c	15	1235	93.9	7498	1	AY330640S3	AY330642 Helicobac
	16	1233	93.8	768	6	CQ846390	CQ846390 Sequence
	17	1233	93.8	768	6	CQ846394	CQ846394 Sequence
	18	1230	93.5	768	6	CQ846382	CQ846382 Sequence
	19	1229	93.5	768	6	CQ846396	CQ846396 Sequence
c	20	1229	93.5	38561	1	AB120423	AB120423 Helicobac
	21	1228	93.4	768	6	CQ846374	CQ846374 Sequence
	22	1227	93.3	768	6	CQ846378	CQ846378 Sequence
	23	1222	92.9	768	6	CQ846380	CQ846380 Sequence
c	24	1207	91.8	5925	1	HPCAI	X70039 H.pylori ca
c	25	1207	91.8	5925	6	A76409	A76409 Sequence 4
c	26	1207	91.8	5925	6	AR099343	AR099343 Sequence
c	27	1207	91.8	5925	6	AR112380	AR112380 Sequence
c	28	1207	91.8	5925	6	AX030324	AX030324 Sequence
c	29	1207	91.8	5925	6	BD000835	BD000835 Helicobac
c	30	1207	91.8	5925	6	BD000839	BD000839 Helicobac
	31	1204	91.6	749	6	CQ846376	CQ846376 Sequence
c	32	1197	91.0	37837	1	AB120419	AB120419 Helicobac
	33	1195	90.9	749	6	CQ846372	CQ846372 Sequence
c	34	1169	88.9	1017	1	AY269155	AY269155 Helicobac
c	35	1151	87.5	1011	1	AY269157	AY269157 Helicobac
	36	1124	85.5	709	1	AY242079	AY242079 Helicobac
	37	1101	83.7	709	1	AY242080	AY242080 Helicobac
c	38	1043	79.3	695	1	AY269156	AY269156 Helicobac
c	39	1028	78.2	695	1	AY269158	AY269158 Helicobac
	40	871	66.2	555	1	AY242081	AY242081 Helicobac
	41	825	62.7	498	1	AY153266	AY153266 Helicobac
	42	824	62.7	498	1	AY153327	AY153327 Helicobac
	43	820	62.4	498	1	AY153267	AY153267 Helicobac
	44	819	62.3	498	1	AY153323	AY153323 Helicobac

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 10, 2006, 17:51:43 ; Search time 619 Seconds  
(without alignments)  
2745.552 Million cell updates/sec

Title: US-10-729-571B-2  
Perfect score: 1315  
Sequence: 1 MKIGVFD SGVGGFSVLKSL.....FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10729571/runat\_09022006\_102147\_17223/app\_query.fasta\_1  
-DB=N\_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h  
-USER=US10729571\_@CGN\_1\_1\_727\_@runat\_09022006\_102147\_17223 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_21:\*

1:	geneseqn1980s:*
2:	geneseqn1990s:*
3:	geneseqn2000s:*
4:	geneseqn2001as:*
5:	geneseqn2001bs:*
6:	geneseqn2002as:*
7:	geneseqn2002bs:*
8:	geneseqn2003as:*
9:	geneseqn2003bs:*
10:	geneseqn2003cs:*
11:	geneseqn2003ds:*
12:	geneseqn2004as:*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1315	100.0	768	12	ADR04137	Adr04137 Helicobac
2	1257	95.6	768	12	ADR04139	Adr04139 Helicobac
3	1248	94.9	765	12	ADR04169	Adr04169 Helicobac
4	1248	94.9	768	4	AAS53601	Aas53601 Helicobac
5	1248	94.9	768	8	ACA34676	Aca34676 Prokaryot
6	1248	94.9	768	12	ADR04155	Adr04155 Helicobac
7	1246	94.8	768	12	ADR04157	Adr04157 Helicobac
8	1240	94.3	768	12	ADR04163	Adr04163 Helicobac
9	1237	94.1	768	12	ADR04141	Adr04141 Helicobac
10	1237	94.1	768	12	ADR04159	Adr04159 Helicobac
11	1233	93.8	768	12	ADR04161	Adr04161 Helicobac
12	1233	93.8	768	12	ADR04165	Adr04165 Helicobac
13	1230	93.5	768	12	ADR04153	Adr04153 Helicobac
14	1229	93.5	768	12	ADR04167	Adr04167 Helicobac
15	1228	93.4	768	12	ADR04145	Adr04145 Helicobac
16	1227	93.3	768	12	ADR04149	Adr04149 Helicobac
17	1222	92.9	768	12	ADR04151	Adr04151 Helicobac
c 18	1207	91.8	5925	2	AAQ48733	Aaq48733 CAI gene.
c 19	1207	91.8	19932	2	AAT46159	Aat46159 CagI locu
20	1204	91.6	749	12	ADR04147	Adr04147 Helicobac
21	1195	90.9	749	12	ADR04143	Adr04143 Helicobac
22	1108	84.3	657	2	AAT68133	Aat68133 H. pylori
23	972	73.9	564	2	AAT67571	Aat67571 H. pylori
24	659	50.1	753	8	ACA30587	Aca30587 Prokaryot
25	415	31.6	765	12	ADR04209	Adr04209 A pyrophi
26	400	30.4	1341	4	ABL52904	Abl52904 Heat-resi
27	373	28.4	804	8	ACA47329	Aca47329 Prokaryot
28	362.5	27.6	792	3	ABK11639	Abk11639 Heat resi
29	362	27.5	801	8	ACA46654	Aca46654 Prokaryot
30	361	27.5	768	4	AAS51328	Aas51328 Enterococ
31	361	27.5	822	12	ADR04179	Adr04179 E faecali
32	361	27.5	828	4	AAS52986	Aas52986 Enterococ
33	360	27.4	798	4	AAS51709	Aas51709 Staphyloc
34	360	27.4	798	8	ACF72881	Acf72881 Staphyloc
35	360	27.4	801	4	AAS55254	Aas55254 Staphyloc
36	360	27.4	801	4	AAS54605	Aas54605 Staphyloc
37	360	27.4	801	8	ACA19705	Aca19705 Prokaryot
38	360	27.4	801	14	ADW94335	Adw94335 Prolifera
39	360	27.4	810	6	ABN91553	Abn91553 Staphyloc
40	360	27.4	810	13	ADS02511	Ads02511 Staphyloc
41	360	27.4	1896	14	ADW94108	Adw94108 Staphyloc
42	355	27.0	822	12	ADH97047	Adh97047 E. faecal
43	355	27.0	822	12	ADH97049	Adh97049 E. faecal
44	355	27.0	822	14	AEC13404	Aec13404 Enterococ
45	355	27.0	822	14	AEC13402	Aec13402 Enterococ



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 10, 2006, 18:22:04 ; Search time 822 Seconds  
(without alignments)  
2565.318 Million cell updates/sec

Title: US-10-729-571B-2  
Perfect score: 1315  
Sequence: 1 MKIGVFD SGVGGFSVLKSL.....FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10729571/runat\_09022006\_102155\_17375/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_Main -QFMT=fastap -SUFFIX=p2n.rnpbm  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext  
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04  
-USER=US10729571\_@CGN\_1\_1\_1026\_@runat\_09022006\_102155\_17375 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query					Description
	No.	Score	Match Length	DB	ID	
	1	1315	100.0	768	7	US-10-335-977-2873
	2	1315	100.0	768	8	US-10-729-571B-1
	3	1257	95.6	768	8	US-10-729-571B-3
	4	1248	94.9	765	8	US-10-729-571B-33
	5	1248	94.9	768	3	US-09-815-242-7238
	6	1248	94.9	768	7	US-10-282-122A-22546
	7	1248	94.9	768	8	US-10-729-571B-19
	8	1246	94.8	768	8	US-10-729-571B-21
	9	1240	94.3	768	8	US-10-729-571B-27
	10	1237	94.1	768	8	US-10-729-571B-5
	11	1237	94.1	768	8	US-10-729-571B-23
	12	1233	93.8	768	8	US-10-729-571B-25
	13	1233	93.8	768	8	US-10-729-571B-29
	14	1230	93.5	768	8	US-10-729-571B-17
	15	1229	93.5	768	8	US-10-729-571B-31
	16	1228	93.4	768	8	US-10-729-571B-9
	17	1227	93.3	768	8	US-10-729-571B-13
	18	1222	92.9	768	8	US-10-729-571B-15
c	19	1207	91.8	5925	3	US-09-921-157-4
	20	1204	91.6	749	8	US-10-729-571B-11
	21	1195	90.9	749	8	US-10-729-571B-7
	22	1108	84.3	657	7	US-10-335-977-2872
	23	972	73.9	564	7	US-10-335-977-2871
	24	659	50.1	753	7	US-10-282-122A-18457
	25	415	31.6	765	8	US-10-729-571B-73
	26	373	28.4	804	7	US-10-282-122A-35199
	27	362	27.5	801	7	US-10-282-122A-34524
	28	361	27.5	768	3	US-09-815-242-3910
	29	361	27.5	822	8	US-10-729-571B-43
	30	361	27.5	828	3	US-09-815-242-6623
	31	360	27.4	798	3	US-09-815-242-4291
	32	360	27.4	801	3	US-09-815-242-8242
	33	360	27.4	801	3	US-09-815-242-8891
	34	360	27.4	801	7	US-10-282-122A-7575
	35	360	27.4	801	8	US-10-857-625-275
	36	360	27.4	810	7	US-10-724-972A-1806
	37	360	27.4	1896	8	US-10-857-625-42
	38	355	27.0	822	9	US-10-953-901-238
	39	355	27.0	822	9	US-10-953-901-240
	40	355	27.0	825	7	US-10-282-122A-6347
	41	355	27.0	11597	3	US-09-070-927A-222
	42	354	26.9	801	8	US-10-729-571B-45
	43	353	26.8	910	5	US-10-221-349-1
c	44	353	26.8	4665	5	US-10-221-349-2
	45	351	26.7	805	3	US-09-974-300-1721

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 10, 2006, 18:02:09 ; Search time 4082 Seconds  
(without alignments)  
2922.760 Million cell updates/sec

Title: US-10-729-571B-2  
Perfect score: 1315  
Sequence: 1 MKIGVFD SGVGGFSVLKSL.....FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10729571/runat\_09022006\_102151\_17277/app\_query.fasta\_1  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h  
-USER=US10729571\_@CGN\_1\_1\_5315\_@runat\_09022006\_102151\_17277 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_htc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			%				ID	Description
	No.	Score	Query	Match	Length	DB		
c	1	261.5	19.9	749	10	CG898169	CG898169	pastbac06
	2	192.5	14.6	934	9	BZ568423	BZ568423	pacs2-164
	3	180	13.7	847	7	CN822800	CN822800	Oa_splbn_
	4	180	13.7	847	7	CO202755	CO202755	Oa_splbn_
	5	180	13.7	857	7	CN824589	CN824589	Oa_splbn_
c	6	177	13.5	818	8	CX954786	CX954786	UMC-bof_0
	7	176	13.4	711	2	BG354824	BG354824	MBTsMLA03
	8	167	12.7	745	7	CN822751	CN822751	Oa_splbn_
	9	167	12.7	750	7	CO202781	CO202781	Oa_splbn_
c	10	162.5	12.4	899	9	BH160828	BH160828	ENTSI47TF
c	11	152	11.6	753	8	DN147359	DN147359	4913_F12_
c	12	144	11.0	716	10	CL681111	CL681111	PRI0130a_
c	13	139	10.6	1124	9	BZ548499	BZ548499	pacs1-60_
	14	137	10.4	1049	9	BZ552420	BZ552420	pacs1-60_
	15	136	10.3	386	1	AW340885	AW340885	xy50a04.x
c	16	133	10.1	270	1	AW419141	AW419141	xy50g05.x
	17	125	9.5	1080	9	BH770578	BH770578	LLMGtag33
	18	115	8.7	794	9	BZ563301	BZ563301	pacs2-164
	19	114	8.7	657	10	CG898106	CG898106	pastbac06
c	20	108	8.2	859	2	BE960437	BE960437	601653169
c	21	97.5	7.4	1024	10	CL039659	CL039659	CH216-48E
	22	97	7.4	888	9	AZ678697	AZ678697	ENTLR73TR
	23	95	7.2	720	6	CD884162	CD884162	F1.115M01
	24	95	7.2	932	6	CA982602	CA982602	AGENCOURT
	25	94.5	7.2	877	9	BZ191089	BZ191089	CH230-424
c	26	94	7.1	550	6	CB829416	CB829416	LjNEST97h
	27	93.5	7.1	896	5	BW640320	BW640320	BW640320
	28	93.5	7.1	1012	5	BU125085	BU125085	603151592
	29	92.5	7.0	549	11	CNS07F4A	AL607996	Anopheles
	30	92.5	7.0	652	9	BH387443	BH387443	AG-ND-142
c	31	92.5	7.0	731	9	BH397141	BH397141	AG-ND-149
	32	92.5	7.0	758	6	CB231653	CB231653	AGENCOURT
	33	92	7.0	274	3	BI883433	BI883433	fn16g11.y
	34	92	7.0	714	8	DN470001	DN470001	USDA-FP_1
	35	91.5	7.0	724	5	BW435594	BW435594	BW435594
c	36	91.5	7.0	928	5	BU129699	BU129699	603116281
	37	91	6.9	723	11	CR040861	CR040861	Reverse s
	38	91	6.9	824	5	BU122315	BU122315	603146981
	39	91	6.9	1030	10	AB080682	AB080682	Finegoldi
	40	90.5	6.9	928	5	BU126137	BU126137	603151437
c	41	90	6.8	547	6	CF100248	CF100248	rv40h02.y
c	42	90	6.8	635	9	BZ392764	BZ392764	EINDN60TF
	43	90	6.8	825	3	BI770124	BI770124	603053305
	44	90	6.8	1062	5	BX403727	BX403727	BX403727
	45	89.5	6.8	611	3	BJ112536	BJ112536	BJ112536